

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:38:30 ; Search time 95 Seconds
(without alignments)
1178.804 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttcgcgagtggtgg.....gctattattagaggagcgaa 63

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/8B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/baCkfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	127	3	US-09-635-132-16
2	33.6	53.3	129	2	US-08-189-256A-25
3	33.6	53.3	129	3	US-09-193-853-25
4	33.6	53.3	140	2	US-08-189-256A-19
5	33.6	53.3	140	3	US-09-193-853-19
6	33.6	53.3	150	2	US-08-189-256A-1
7	33.6	53.3	150	3	US-09-193-853-1
8	33.6	53.3	161	2	US-08-189-256A-18
9	33.6	53.3	161	3	US-09-193-853-18
10	33.6	53.3	164	2	US-08-189-256A-26
11	33.6	53.3	164	3	US-09-193-853-26
12	33.6	53.3	165	2	US-08-189-256A-4
13	33.6	53.3	165	3	US-09-193-853-4
14	33.6	53.3	168	2	US-08-189-256A-2
15	33.6	53.3	168	3	US-09-193-853-2
16	33.6	53.3	168	3	US-09-351-123-5
17	33.6	53.3	184	3	US-09-283-419-3
18	33.6	53.3	201	3	US-09-011-336-58
19	33.6	53.3	202	3	US-09-843-324A-1
20	33.6	53.3	244	3	US-09-351-123-6
21	33.6	53.3	244	3	US-09-843-324A-2
22	33.6	53.3	258	2	US-08-189-256A-24
23	33.6	53.3	258	3	US-09-193-853-24
24	33.6	53.3	300	3	US-09-202-316-4

Sequence 7, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 28, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 63, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 19, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 32, Appl
Sequence 1, Appli

US-09-635-132-16
Sequence 16, Application US/09635132
Patent No. 6620601
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, ISAMU
APPLICANT: NAKASHITA, HIDEO
APPLICANT: YOSHIOKA, KEIKO
APPLICANT: DOI, YOSHIOHARU
TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED
FILE REFERENCE: 081356/0148
CURRENT APPLICATION NUMBER: US/09/635,132
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: JP 11-225832
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: JP 11-225839
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 127
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-635-132-16

Query Match 53.3%; Score 33.6; DB 3; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.0011;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 53 GTGGGATTGACGTGAGGGGGGAGGGATGCGCTATATTCTGGGAGCGAA 100

RESULT 2
US-08-189-256A-25
Sequence 25, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan

ALIGNMENTS

RESULT 1
US-09-635-132-16
Sequence 16, Application US/09635132
Patent No. 6620601
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, ISAMU
APPLICANT: NAKASHITA, HIDEO
APPLICANT: YOSHIOKA, KEIKO
APPLICANT: DOI, YOSHIOHARU
TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED
FILE REFERENCE: 081356/0148
CURRENT APPLICATION NUMBER: US/09/635,132
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: JP 11-225832
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: JP 11-225839
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 127
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-635-132-16

Query Match 53.3%; Score 33.6; DB 3; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.0011;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 53 GTGGGATTGACGTGAGGGGGGAGGGATGCGCTATATTCTGGGAGCGAA 100

RESULT 2
US-08-189-256A-25
Sequence 25, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan

```
;
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-25

Query Match 53.3%; Score 33.6; DB 2; Length 129;
Best Local Similarity 81.2%; Pred. No. 0.0011;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 46 GTGGGATTGACGTGAGGGGCGCAGGGATGGCTATATTCTGGAGCGAA 93

RESULT 3
US-09-193-853-25
; Sequence 25, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA

;
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-19

Query Match 53.3%; Score 33.6; DB 3; Length 129;
Best Local Similarity 81.2%; Pred. No. 0.0011;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 46 GTGGGATTGACGTGAGGGGCGCAGGGATGGCTATATTCTGGAGCGAA 93

RESULT 4
US-08-189-256A-19
; Sequence 19, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
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; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-19

Query Match 53.3%; Score 33.6; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGGGAGCGAA 63
|||||
Db 57 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGGAGCGAA 104

RESULT 5

US-09-193-853-19
; Sequence 19, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; Transforming Plastids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-19

Query Match 53.3%; Score 33.6; DB 3; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGGGAGCGAA 63
|||||
Db 57 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGGAGCGAA 104

RESULT 6

US-08-189-256A-1
; Sequence 1, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; Transforming Plastids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-1

Query Match 53.3%; Score 33.6; DB 2; Length 150;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
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DB 41 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTTCTGGAGCGAA 88
|||||

RESULT 7

US-09-193-853-1

; Sequence 1, Application US/09193853

; Patent No. 6388168

; GENERAL INFORMATION:

; APPLICANT: Maliga, Pal

; APPLICANT: Svab, Zora

; APPLICANT: Staub, Jeffrey

; APPLICANT: Zoubenko, Oleg V.

; APPLICANT: Allison, Lori A.

; APPLICANT: Carrer, Helaine

; APPLICANT: Kanevski, Ivan

; TITLE OF INVENTION: DNA Constructs and Methods for Stably

; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

; TITLE OF INVENTION: Expressing Recombinant Proteins Therein

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dann, Dorfman, Herrell and Skillman

; STREET: 1601 Market Street Suite 720

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103-2307

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/193,853

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/189,256

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/518,763

; FILING DATE: 01-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Janet E.

; REGISTRATION NUMBER: 36,252

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 563-4100

; TELEFAX: (215) 563-4044

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 150 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-193-853-1

Query Match 53.3%; Score 33.6; DB 3; Length 150;
Best Local Similarity 81.2%; Pred. No. 0.0012;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
DB 41 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTTCTGGAGCGAA 88
|||||

RESULT 8

US-08-189-256A-18

; Sequence 18, Application US/08189256A

; Patent No. 5877402

; GENERAL INFORMATION:

; APPLICANT: Maliga, Pal

; APPLICANT: Svab, Zora

; APPLICANT: Staub, Jeffrey

; APPLICANT: Zoubenko, Oleg V.

; APPLICANT: Allison, Lori A.

; APPLICANT: Carrer, Helaine

; APPLICANT: Kanevski, Ivan

; TITLE OF INVENTION: DNA Constructs and Methods for Stably

; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

; TITLE OF INVENTION: Expressing Recombinant Proteins Therein

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dann, Dorfman, Herrell and Skillman

; STREET: 1601 Market Street Suite 720

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103-2307

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/189,256A

; FILING DATE: 31-JAN-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/111,398

; FILING DATE: 25-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/518,763

; FILING DATE: 01-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Janet E.

; REGISTRATION NUMBER: 36,252

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 563-4100

; TELEFAX: (215) 563-4044

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 161 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-189-256A-18

Query Match 53.3%; Score 33.6; DB 2; Length 161;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
DB 63 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTTCTGGAGCGAA 110
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RESULT 9

US-09-193-853-18

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; Sequence 18, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09193,853
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-18

Query Match 53.3%; Score 33.6; DB 3; Length 161;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 63 GTGGGATTGACGTGAGGGGCGAGGGATGGCTATATTCTGGGAGCGAA 110

RESULT 10
US-08-189-256A-26
; Sequence 26, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-18

Query Match 53.3%; Score 33.6; DB 3; Length 161;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 63 GTGGGATTGACGTGAGGGGCGAGGGATGGCTATATTCTGGGAGCGAA 110
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; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-26

Query Match 53.3%; Score 33.6; DB 2; Length 164;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 46 GTGGGATTGACGTGAGGGGCGAGGGATGGCTATATTCTGGGAGCGAA 93

RESULT 11
US-09-193-853-26
; Sequence 26, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
```

STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-26

Query Match 53.3%; Score 33.6; DB 3; Length 164;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
|||||
Db 46 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTTCTGGGAGCGAA 93
|||||

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RESULT 12
US-08-189-256A-4
; Sequence 4, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/189,256/
/ PILING DATE: 31-JAN-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/111,398
/ FILING DATE: 25-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/518,763
/ FILING DATE: 01-MAY-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Reed, Janet E.
/ REGISTRATION NUMBER: 36,252
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 563-4100
/ TELEFAX: (215) 563-4044
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 165 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-189-256-4

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Query Match 53.3%; Score 33.6; DB 2; Length 165;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

Dp 41 GTGGGATTGACCTGAGGGGCGAGGGATGGCTATATTTCTGGGAGCGAA 88

RESULT 13
US-09-193-853-4
Sequence 4, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carner, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193.853
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-4

Query Match 53.3%; Score 33.6; DB 3; Length 165;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 41 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 88

RESULT 14

US-08-189-256A-2
Sequence 2, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-2

Query Match 53.3%; Score 33.6; DB 2; Length 168;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 41 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 88

RESULT 15

US-09-193-853-2
Sequence 2, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-2

Query Match

53.3%; Score 33.6; DB 3; Length 168;

Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
|||
Db 41 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCTGGGAGCGAA 88
|||

Search completed: February 21, 2006, 05:40:12
Job time : 95 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:41:51 ; Search time 410 Seconds
(without alignments)
326.188 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttcgcgagtgagg.....gctatttagaggagcgaa 63

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Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New.*
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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	33.6	53.3	2569	9	US-11-190-122-3
3	33.6	53.3	2800	9	US-11-190-122-1
4	33.6	53.3	3119	9	US-11-190-122-2
5	33.6	53.3	5834	7	US-10-527-048-15
6	33.6	53.3	6465	7	US-10-527-048-25
7	33.6	53.3	6659	7	US-10-527-048-22
8	33.6	53.3	7549	7	US-10-527-048-24
9	25.6	40.6	562	6	US-09-925-065A-935299
10	25.6	40.6	562	6	US-09-925-065A-935300
11	25.6	40.6	562	6	US-09-925-065A-952905
12	25.6	40.6	562	6	US-09-925-065A-952906
13	25.6	40.6	624	6	US-09-925-065A-952906
14	25.6	40.6	56054	8	US-10-995-561-13402
15	24.2	38.4	561	6	US-09-925-065A-753058
16	24.2	38.4	561	6	US-09-925-065A-824463
17	24.2	38.4	594	6	US-09-925-065A-308387
18	24.2	38.4	594	6	US-09-925-065A-308388
19	24.2	38.4	594	6	US-09-925-065A-308389
20	24.2	38.4	615	6	US-09-925-065A-753057

21	24.2	38.4	615	6	US-09-925-065A-824462	Sequence 824462,
22	24.2	38.4	2189	9	US-11-072-512-1716	Sequence 1716, Ap
23	24	38.1	537	6	US-09-925-065A-513697	Sequence 513697,
24	24	38.1	607	6	US-09-925-065A-926199	Sequence 926199,
25	24	38.1	607	6	US-09-925-065A-948723	Sequence 948723,
26	23.8	37.8	608	6	US-09-925-065A-539617	Sequence 539617,
27	23.8	37.8	608	6	US-09-925-065A-539618	Sequence 539618,
28	23.8	37.8	629	6	US-09-925-065A-519220	Sequence 519220,
29	23.8	37.8	2034	6	US-09-925-065A-36107	Sequence 36107, A
30	23.8	37.8	2102	6	US-09-925-065A-40864	Sequence 40864, A
31	23.8	37.8	2102	6	US-09-925-065A-40865	Sequence 40865, A
32	23.8	37.8	2644	6	US-09-925-065A-725519	Sequence 725519,
33	23.6	37.5	431	6	US-09-925-065A-587132	Sequence 587132,
34	23.6	37.5	642	6	US-09-925-065A-67485	Sequence 67485, A
35	23.6	37.5	642	6	US-09-925-065A-67486	Sequence 67486, A
36	23.4	37.1	586	6	US-09-925-065A-231	Sequence 231, App
37	23.4	37.1	645	6	US-09-925-065A-864288	Sequence 864288,
38	23.4	37.1	98345	12	US-11-112-908-36	Sequence 36, Appl
39	23.2	36.8	1462	6	US-09-925-065A-86646	Sequence 86646, A
40	23.2	36.8	1462	6	US-09-925-065A-86647	Sequence 86647, A
41	23.2	36.8	1462	6	US-09-925-065A-86648	Sequence 86648, A
42	23.2	36.8	2424	8	US-10-909-125-831	Sequence 831, App
43	23.2	36.8	163162	12	US-11-121-086-66	Sequence 66, Appl
44	23	36.5	591	6	US-09-925-065A-783808	Sequence 783808,
45	23	36.5	2136	6	US-09-925-065A-705163	Sequence 705163,

ALIGNMENTS

RESULT 1
US-10-527-048-14
; Sequence 14, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/527,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: fragment codifying for the promoter region of the plastid 16S
; OTHER INFORMATION: ribosomal RNA (Prn), with added restriction sites.
US-10-527-048-14

Query Match 53.3%; Score 33.6; DB 7; Length 176;
Best Local Similarity 81.2%; Pred. No. 0.0028;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGAGGCGCAA 63
|||||
Db 56 GTGGATTGACCTGAGGGGCGAGGATGCTATATTTCTGGGAGCGAA 103
|||||

RESULT 2

US-11-190-122-3
; Sequence 3, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26

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, , PRIOR APPLICATION NUMBER: 10/500,351
, , PRIOR FILING DATE: 2004-06-25
, , PRIOR APPLICATION NUMBER: pct/us2003/021157
, , PRIOR FILING DATE: 2003-07-03
, , PRIOR APPLICATION NUMBER: 60/590,848
, , PRIOR FILING DATE: 2004-07-23
, , PRIOR APPLICATION NUMBER: 60/590,751
, , PRIOR FILING DATE: 2004-07-23
, , PRIOR APPLICATION NUMBER: 10/519,821
, , PRIOR FILING DATE: 2004-12-30
, , PRIOR APPLICATION NUMBER: 60/400,816
, , PRIOR FILING DATE: 2002-08-02
, , PRIOR APPLICATION NUMBER: 60/393,651
, , PRIOR FILING DATE: 2002-07-03
, , PRIOR APPLICATION NUMBER: 60/393,428
, , PRIOR FILING DATE: 2002-07-03
, , PRIOR APPLICATION NUMBER: pct/us2002/041503
, , PRIOR FILING DATE: 2002-12-26
, , NUMBER OF SEQ ID NOS: 21
, , SOFTWARE: Patentin version 3.2
, , SEQ ID NO 3
, , LENGTH: 2569
, , TYPE: DNA
, , ORGANISM: ARTIFICIAL
, , FEATURE:
, , OTHER INFORMATION: apha-6/nptII expression
US-11-190-122-3

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; FEATURE:
; OTHER INFORMATION: aadA/BADH expression cassette
; US-11-190-122-1

Query Match 53.3%; Score 33.6; DB 9; Length 2800;
Best Local Similarity 81.2%; Pred. No. 0.004;
Matches 39; Conservative 0; Mismatches 9; Indels 0

Qy 16 GTGGGATTGACGTAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
Db 125 GTGGGATTGACGTAGGGGGCGAGGGATGGCTATATTCTGGGAGCGAA 172
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|||||

RESULT 4
US-11-190-122-2
; Sequence 2, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Emb
; FILE REFERENCE: CHU-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 3119
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: gfp/BADH expression cassette
; US-11-190-122-2

Query Match 53.3%; Score 33.6; DB 9; Length 3119;
Best Local Similarity 81.2%; Pred. No. 0.0041;
Matches 39; Conservative 0; Mismatches 9; Indels 0

Qy 16 GTGGGATTGACGTAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
Db 119 GTGGGATTGACGTAGGGGGCGAGGGATGGCTATATTCTGGGAGCGAA 166
|||||
|||||

RESULT 5
US-10-527-048-15
; Sequence 15, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPL
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/527,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26

```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 5834

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA between the rice atpB and
; OTHER INFORMATION: tobacco rbcl borders.
US-10-527-048-15

Query Match 53.3%; Score 33.6; DB 7; Length 5834;

Best Local Similarity 81.2%; Pred. No. 0.0044;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 2005

RESULT 6

US-10-527-048-25

; Sequence 25, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 6465

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA-Bar between the rice atpB and
; OTHER INFORMATION: tobacco rbcl borders.
US-10-527-048-25

Query Match 53.3%; Score 33.6; DB 7; Length 6465;

Best Local Similarity 81.2%; Pred. No. 0.0044;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 2005

RESULT 7

US-10-527-048-22

; Sequence 22, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 6659

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA-aada between the rice atpB and
; OTHER INFORMATION: tobacco rbcl borders.
US-10-527-048-22

Query Match 53.3%; Score 33.6; DB 7; Length 6659;

Best Local Similarity 81.2%; Pred. No. 0.0045;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 2005

RESULT 8

US-10-527-048-24

; Sequence 24, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 7549

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DN
; OTHER INFORMATION: fragment from the vector pVTPA-HB-aada between the rice atpB .
; OTHER INFORMATION: tobacco rbcl borders.
US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 7549;

Best Local Similarity 81.2%; Pred. No. 0.0045;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 2848 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 2895

RESULT 9

US-09-925-065A-935299

; Sequence 935299, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 935299

; LENGTH: 562

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-935299

Query Match 40.6%; Score 25.6; DB 6; Length 562;

Best Local Similarity 66.1%; Pred. No. 3.5;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

US-09-925-065A-693983

Query Match 40.6%; Score 25.6; DB 6; Length 624;
Best Local Similarity 66.1%; Pred. No. 3.5;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGG 56
|||||
Db 445 GAGCCCTTCTCCGGCTGGCTGAGGCTGAGCGGGCTCCCTCGGCTTGTGGGGAGG 500
|||||

RESULT 14

US-10-995-561-13402
; Sequence 13402, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13402
; LENGTH: 56054
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(56054)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13402

Query Match 40.6%; Score 25.6; DB 8; Length 56054;
Best Local Similarity 66.1%; Pred. No. 6.2;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGG 56
|||||
Db 5170 GAGCCCTTCTCTGGGCTGGCTAGTCCGAGCGGGCTCCCTCGGCTTGTGGGGAGG 5225
|||||

RESULT 15

US-09-925-065A-753058
; Sequence 753058, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 753058
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-753058

Query Match 38.4%; Score 24.2; DB 6; Length 561;
Best Local Similarity 66.0%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAG 53
|||||
Db 254 GAGCCCTTCTCTGGGCTGGCGGAGGCTGAGCCGGCTCCCTCAGCTTGGTTTG 306
|||||

Search completed: February 21, 2006, 06:33:19
Job time : 411 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:40:29 ; Search time 492 Seconds
(without alignments)
1058.884 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63
Sequence: 1 gagctctctccagggtggg.....gctatattaggaggcgaa 63

Scoring table: IDENTITY NUC
Gapop 10^0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	8	US-10-737-251-51
2	38.4	61.0	112	8	US-10-737-251-18
3	38.4	61.0	112	8	US-10-737-251-19
4	38.4	61.0	112	8	US-10-737-251-23
5	36.6	58.1	112	8	US-10-737-251-10
6	34.8	55.2	112	8	US-10-737-251-9
7	33.6	53.3	112	8	US-10-737-251-3
8	33.6	53.3	112	8	US-10-737-251-4
9	33.6	53.3	112	8	US-10-737-251-5
10	33.6	53.3	112	8	US-10-737-251-6
11	33.6	53.3	112	8	US-10-737-251-7
12	33.6	53.3	112	8	US-10-737-251-8
13	33.6	53.3	112	8	US-10-737-251-27
14	33.6	53.3	112	8	US-10-737-251-28
15	33.6	53.3	112	8	US-10-737-251-29
16	33.6	53.3	112	8	US-10-737-251-30
17	33.6	53.3	119	8	US-10-881-813-6
18	33.6	53.3	202	3	US-09-843-324A-1
19	33.6	53.3	220	7	US-10-095-514-3
20	33.6	53.3	233	8	US-10-737-251-38
21	33.6	53.3	234	8	US-10-737-251-42
22	33.6	53.3	244	3	US-09-843-324A-2
23	33.6	53.3	1143	6	US-10-460-716-2

ALIGNMENTS

RESULT 1
US-10-737-251-51
; Sequence 51, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Prmn
US-10-737-251-51

Query Match 100.0%; Score 63; DB 8; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCTTCTCCGAGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGC 60
|||
Db 1 GAGCTCTTCTCCGAGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGC 60

QY 61 GAA 63
|||
Db 61 GAA 63

RESULT 2
US-10-737-251-18
; Sequence 18, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Prmn
US-10-737-251-51

Sequence 3, Appli
Sequence 4, Appli
Sequence 26, Appl
Sequence 63, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 19, Appl
Sequence 4, Appli
Sequence 1, Appli
Sequence 41, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 16, Appl
Sequence 43, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 19, Appl
Sequence 13, Appl

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; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-18

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGGCTCCGATGGCTATATTCTGGGAGCGAA 75

RESULT 3
US-10-737-251-19
; Sequence 19, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-19

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGGCTCCGATGGCTATATTCTGGGAGCGAA 75

RESULT 4
US-10-737-251-23
; Sequence 23, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 23
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-23

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTAGAGGAGCGAA 75

RESULT 5
US-10-737-251-10
; Sequence 10, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-10

Query Match      58.1%; Score 36.6; DB 8; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 13 GAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 25 GAGGTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTGGGAGCGAA 75

RESULT 6
US-10-737-251-9
; Sequence 9, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-9
```

```
Query Match      55.2%; Score 34.8; DB 8; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.00064;
Matches 42; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 10 TCCGAGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 22 TCCCTCGTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 7
US-10-737-251-3
; Sequence 3, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-3

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 8
US-10-737-251-4
; Sequence 4, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-4

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75
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```
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 9
US-10-737-251-5
; Sequence 5, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-5

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 10
US-10-737-251-6
; Sequence 6, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-6

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 11
US-10-737-251-7
; Sequence 7, Application US/10737251
; Publication No. US20040221338A1
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```

; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-7

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 12
US-10-737-251-8
; Sequence 8, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-8

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 13
US-10-737-251-27
; Sequence 27, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251

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; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-27

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 14
US-10-737-251-28
; Sequence 28, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-28

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 15
US-10-737-251-29
; Sequence 29, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 112

```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prm promoter derivative
US-10-737-251-29

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGCGCAA 63
        |||||
Db      28 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGCGCAA 75
        |||||

Search completed: February 21, 2006, 05:48:49
Job time : 493 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:37:59 ; Search time 3773 Seconds
(without alignments)
781.231 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctctctccagggtggg.....gctatattaggaggcgaa 63

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hrc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32	50.8	243	9	BH009665 ef31f05.x
2	32	50.8	295	9	BZ457960 BOND72TR
3	32	50.8	380	7	CN859023 000728AAA
4	32	50.8	395	9	BH678911 BOMDD83TR
5	32	50.8	415	7	CN930271 000322AFB
6	32	50.8	498	7	CN872595 020807AAP
7	32	50.8	510	1	AJ876197 AJ876197
8	32	50.8	561	9	BH522564 BQGRW45TF
9	32	50.8	598	7	CN871707 010128AAP
C 10	32	50.8	734	10	CG026772 PGAAE374TR
C 11	32	50.8	764	10	CG026604 PGAAE307TF
C 12	32	50.8	825	9	BZ498361 BONLE43TF
C 13	30.4	48.3	169	9	AQ962940 LERGI42TR
C 14	30.4	48.3	183	9	BZ483881 BOAGI129TR
C 15	30.4	48.3	194	9	AQ962945 LERGI45TR
16	30.4	48.3	199	9	BH537952 BOGFU38TR
17	30.4	48.3	238	9	BH677595 BOMCM49TR
18	30.4	48.3	244	9	BH588286 BOGFU54TF
19	30.4	48.3	292	9	BH474703 BOCQI49TF
20	30.4	48.3	299	9	BZ507339 BONPU16TF
21	30.4	48.3	305	8	DT034079 VIL089A04
C 22	30.4	48.3	305	9	BH646726 BQGRW48TF

23	30.4	48.3	322	9	BH705426
24	30.4	48.3	326	9	BZ440851
25	30.4	48.3	337	9	BZ464817
26	30.4	48.3	344	9	BZ476987
27	30.4	48.3	361	9	BZ470963
28	30.4	48.3	364	9	BH558977
29	30.4	48.3	367	9	BH430502
30	30.4	48.3	368	9	BH493122
31	30.4	48.3	396	9	BH630640
32	30.4	48.3	405	9	BH427396
33	30.4	48.3	407	9	BZ489878
C 34	30.4	48.3	410	9	BH549701
35	30.4	48.3	416	9	BH664090
36	30.4	48.3	419	9	BH662193
37	30.4	48.3	422	9	BH475597
38	30.4	48.3	423	9	BH653681
39	30.4	48.3	426	9	AQ968706
40	30.4	48.3	434	9	BH545732
41	30.4	48.3	434	9	BH678091
42	30.4	48.3	435	9	BZ447238
43	30.4	48.3	440	9	BH543946
44	30.4	48.3	441	9	BH657205
45	30.4	48.3	441	9	CC966698

ALIGNMENTS

RESULT 1
BH009665/c

LOCUS

DEFINITION ef31f05.x1 TO1000 Brassica oleracea genomic clone ef31f05 5', genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH009665 243 bp DNA linear GSS 04-MAY-2001
ef31f05.x1 TO1000 Brassica oleracea genomic clone ef31f05 5',
genomic survey sequence.

BH009665
BH009665.1 GI:13955602
GSS.

Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 243)
Katarai, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J.,
Baliya, V., Bell, M., Cunnius, D.M., King, L., Kirchoff, K., Kuit, K.,
Miller, B., Nascimeto, L., Preston, R., Rodriguez, S., Santos, L.,
Shah, R., Vil, M.D., Zutavern, T., Bal, H., Dedhia, N. and McCombie, W.R.

Whole Genome Shotgun Reads from Brassica oleracea
Unpublished (2001)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: ef31 row: f column: 05
Seq primer: -21fwdUniv
Class: shotgun
High quality sequence stop: 243.

Location/Qualifiers
1. .243
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="ef31f05"
/notes="Vector: M13 for .x reads, pzero-2 for .b and .g
reads; Site 1: EcoRV; DNA prepared as whole genome shotgun
library from young, green leaves. May contain some plasmid
DNAs. DNA provided by Dr. Tom Osborn, University of
Wisconsin-Madison, Department of Agronomy."

source
Location/Qualifiers
1. .243
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="ef31f05"
/notes="Vector: M13 for .x reads, pzero-2 for .b and .g
reads; Site 1: EcoRV; DNA prepared as whole genome shotgun
library from young, green leaves. May contain some plasmid
DNAs. DNA provided by Dr. Tom Osborn, University of
Wisconsin-Madison, Department of Agronomy."

ORIGIN

```

Query Match      50.8%; Score 32; DB 9; Length 243;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 97 GTGGGATTGACGTGAGGGGTACGGGTAGCTATATTCTGGGAGCGAA 50
|||||

RESULT 2
BZ457960
LOCUS BOND72TR BO_1.6.2_KB_tot Brassica oleracea genomic clone BOND72,
DEFINITION genomic survey sequence.
ACCESSION BZ457960
VERSION BZ457960.1 GI:26737897
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 295)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..295
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOND72"
/clone_lib="BO_1.6.2_KB_tot"
/note="Vector: pHOS1; Site 1: BatXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BatXI linkers"

ORIGIN
Query Match      50.8%; Score 32; DB 9; Length 295;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 199 GTGGGATTGACGTGAGGGGTACGGGTAGCTATATTCTGGGAGCGAA 246
|||||

RESULT 3
CN859023
LOCUS 000728AAAA008805HT (AAAA) Royal Gala 59 DAFB fruit, seeds removed
DEFINITION Malus x domestica cDNA clone AAAA008805, mRNA sequence.
ACCESSION CN859023
VERSION CN859023.1 GI:48114953
KEYWORDS EST.
SOURCE Malus x domestica
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 380)

```

```

AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1..380
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAAA008805"
/tissue_type="fruit"
/dev stage="59 days after full bloom, seeds removed"
/clone_lib="(AAAA) Royal Gala 59 DAFB fruit, seeds
removed"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN
Query Match      50.8%; Score 32; DB 7; Length 380;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 285 GTGGGATTGACGTGAGGGGTAGGATGGCTATATTCTGGGAGCGAA 332
|||||

RESULT 4
BH678911
LOCUS BOMDD83TR BO_2.3_KB Brassica oleracea genomic clone BOMDD83,
DEFINITION genomic survey sequence.
ACCESSION BH678911
VERSION BH678911.1 GI:18749354
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 395)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..395
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMDD83"
/clone_lib="BO_2.3_KB"
/note="Vector: pHOS1; Site 1: BatXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

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ORIGIN

Query Match 50.8%; Score 32; DB 9; Length 395;
 Best Local Similarity 79.2%; Pred. No. 1.1;
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 92 GTGGGATTGACGTGAGGGGGTACGGGTAGCTATATTCTGGAGCGAA 139
 |||||

RESULT 5

LOCUS CN930271 415 bp mRNA linear EST 07-JUN-2004
 DEFINITION 000322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA clone AFBC002396, mRNA sequence.

ACCESSION CN930271
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE

AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
 TITLE HortResearch Apple EST Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Gleave, A.
 Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 Email: est@hortresearch.co.nz.

FEATURES

source
 1. 415
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="AFBC002396"
 /tissue_type="Floral bud"
 /dev_stage="Pre-opening, flower at stage of nectar/pollen
 formation"
 /clone_lib="(AFBC) Royal Gala pre-opened floral bud"
 /note="Vector: pBK-CMV; Library sequenced by Genesis
 Research & Development"

ORIGIN

Query Match 50.8%; Score 32; DB 7; Length 415;
 Best Local Similarity 79.2%; Pred. No. 1.1;
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 236 GTGGGATTGACGTGAGGGGGTACGGGTAGCTATATTCTGGAGCGAA 283
 |||||

RESULT 6

LOCUS CN872595 498 bp mRNA linear EST 04-JUN-2004
 DEFINITION 020807AAPA005328HT (AAPA) Royal Gala 24 DAFB fruit Malus x domestica cDNA clone AAPA005328, mRNA sequence.

ACCESSION CN872595
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.
 1 (bases 1 to 498)

AUTHORS

Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
 TITLE HortResearch Apple EST Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Gleave, A.
 Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 Email: est@hortresearch.co.nz.

FEATURES

source
 1. 498
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="AAPA005328"
 /tissue_type="Fruit"
 /dev_stage="24 days after full bloom"
 /clone_lib="(AAPA) Royal Gala 24 DAFB fruit"
 /note="Vector: pBK-CMV; Library sequenced by Genesis
 Research & Development"

ORIGIN

Query Match 50.8%; Score 32; DB 7; Length 498;
 Best Local Similarity 79.2%; Pred. No. 1.1;
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 287 GTGGGATTGACGTGAGGGGGTACGGGTAGCTATATTCTGGAGCGAA 334
 |||||

RESULT 7

LOCUS AJ876197/c 510 bp mRNA linear EST 17-FEB-2005
 DEFINITION bloom Prunus persica fruit mesocarp plus epidermis 80 days after
 Prunus persica cDNA clone PR0213A05, mRNA sequence.

ACCESSION AJ876197
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Prunus persica (peach)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 510)

REFERENCE

AUTHORS Le Dantec, L., Cosson, P., Renaud, C., Garcia, V., Dumoulin, P.,
 Rothan, C., Filippi, G., Laigret, F., Moing, A. and Dirlewanger, E.
 TITLE Peach (Prunus persica (L.) Batsch) fruit ESTs from two early
 development stages
 JOURNAL Unpublished (2004)
 COMMENT Contact: Le Dantec L
 Ureiv, Inra, INRA, Centre de Bordeaux
 BP 81 Villenave d'Ornon Cedex, 33 883, FRANCE.

FEATURES

source
 1. 510
 /organism="Prunus persica"
 /mol_type="mRNA"
 /cultivar="Fantasia"
 /db_xref="taxon:3760"
 /clone="PR0213A05"
 /tissue_type="fruit mesocarp plus epidermis"
 /dev_stage="80 days after bloom"
 /clone_lib="Prunus persica fruit mesocarp plus epidermis
 80 days after bloom"

ORIGIN

Query Match 50.8%; Score 32; DB 1; Length 510;
 Best Local Similarity 79.2%; Pred. No. 1.1;
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

```

Db      262 GTGGGATTGACGTGAGGGGTAGGATGGCTATATTTCTGGAGCGAA 215
|||||
RESULT 8
BH522564
LOCUS   561 bp      DNA      linear      GSS 13-DEC-2001
DEFINITION BOGRW45TF BOGR Brassica oleracea genomic clone BOGRW45, genomic
survey sequence.
ACCESSION BH522564
VERSION   BH522564.1 GI:17730649
KEYWORDS GSS.
SOURCE   Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 561)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE   Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BOGRW45TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..561
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGRW45"
/clone_lib="BOGR"
/notes="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

FEATURES
source
Query Match 50.8%; Score 32; DB 9; Length 561;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGTCCCTAGGCTATATTAGAGGGAGCGAA 63
|||||
Db 419 GTGGGATTGACGTGAGGGGTACGGGTAGCTATATTTCTGGAGCGAA 466
|||||

RESULT 9
CN871707
LOCUS   598 bp      mRNA      linear      EST 04-JUN-2004
DEFINITION O10128AAPA001324HT (AAPA) Royal Gala 24 DAFB fruit Malus x
domestica cDNA AAPA001324, mRNA sequence.
ACCESSION CN871707
VERSION   CN871707.1 GI:48257865
KEYWORDS EST.
SOURCE   Malus x domestica
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 598)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,B. and Yauk,Y.
HortResearch Apple EST Project
TITLE   HortResearch Apple EST Project
JOURNAL Unpublished (2004)

COMMENT Contact: Gleave,A.
Sequencing facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1..598
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAPA001324"
/tissue_type="Fruit"
/dev_stage="24 days after full bloom"
/clone_lib="(AAPA) Royal Gala 24 DAFB fruit"
/notes="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

FEATURES
source
Query Match 50.8%; Score 32; DB 7; Length 598;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

ORIGIN
16 GTGGGATTGACGTGAGGGGTCCCTAGGCTATATTAGAGGGAGCGAA 63
|||||
423 GTGGGATTGACGTGAGGGGTAGGATGGCTATATTTCTGGAGCGAA 470
|||||

RESULT 10
CG026772/c
LOCUS   734 bp      DNA      linear      GSS 19-AUG-2003
DEFINITION PGAB74TR PGAA Carica papaya genomic clone PGAB74, genomic survey
sequence.
ACCESSION CG026772
VERSION   CG026772.1 GI:33899928
KEYWORDS GSS.
SOURCE   Carica papaya (papaya)
ORGANISM Carica papaya
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Caricaceae; Carica.
REFERENCE 1 (bases 1 to 734)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE   Whole genome shotgun sequencing of Carica papaya
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PGAB74TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA provided by Ray Ming was isolated from cultivar SunUp that was
transgenic for papaya ringspot virus coat protein gene
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..734
/organism="Carica papaya"
/mol_type="genomic DNA"
/cultivar="SunUp"
/db_xref="taxon:3649"
/clone="PGAB74"
/clone_lib="PGAA"
/notes="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

FEATURES
source
Query Match 50.8%; Score 32; DB 10; Length 734;
Best Local Similarity 79.2%; Pred. No. 1.2;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

ORIGIN
16 GTGGGATTGACGTGAGGGGTCCCTAGGCTATATTAGAGGGAGCGAA 63
|||||
423 GTGGGATTGACGTGAGGGGTAGGATGGCTATATTTCTGGAGCGAA 470
|||||

```

Qy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 114 GTGGATTGACGTGAGGGGCTAGGATGGCTATATTCTGGGAGCGAA 67
 |||||

RESULT 11
 CG026604/c
 LOCUS
 DEFINITION PGAAE30TF PGAA Carica papaya genomic clone PGAAE30, genomic survey sequence.
 ACCESSION CG026604
 VERSION CG026604.1 GI:33898760
 KEYWORDS GSS.
 SOURCE Carica papaya (papaya)
 ORGANISM Carica papaya
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Caricaceae; Carica.
 1 (bases 1 to 764)
 Town, C.D., Van Aken, S., Utterbach, T. and Fraser, C.M.
 Whole genome shotgun sequencing of Carica papaya
 Unpublished (2003)
 Other_GSSs: PGAAE30TF
 Contact: Chris Town
 TIGR

7712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA provided by Ray Ming was isolated from cultivar SunUp that was transgenic for papaya ringspot virus coat protein gene
 Seq primer: TF
 Class: sheared ends.

FEATURES

source

Location/Qualifiers

1..764

/organism="Carica papaya"

/mol_type="genomic DNA"

/cultivar="SunUp"

/db_xref="taxon:3649"

/clones="PGAAE30"

/clone_lib="PGAA"

/note="vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 50.8%; Score 32; DB 10; Length 764;
 Best Local Similarity 79.2%; Pred. No. 1.2;
 Matches 36; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 622 GTGGATTGACGTGAGGGGCTAGGATGGCTATATTCTGGGAGCGAA 575
 |||||

RESULT 12
 BZ498361
 LOCUS
 DEFINITION BONLE43TF BO 1.6.2 KB tot Brassica oleracea genomic clone BONLE43, genomic survey sequence.
 ACCESSION BZ498361
 VERSION BZ498361.1 GI:27012539
 KEYWORDS GSS.
 SOURCE Brassica oleracea

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 825)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

Utterbach, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490
 PUBMED
 COMMENT
 Other_GSSs: BONLE43TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES

source

Location/Qualifiers

1..825

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="T01000DH3"

/db_xref="taxon:3712"

/clones="BONLE43"

/clone_lib="BO 1.6.2 KB tot"

/note="vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared

total DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 50.8%; Score 32; DB 9; Length 825;
 Best Local Similarity 79.2%; Pred. No. 1.2;
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 4 GTGGATTGACGTGAGGGGTTTGGGTAGCTATATTCTGGGAGCGAA 51
 |||||

RESULT 13

LOCUS

AQ962940/c

DEFINITION

LERGI42TR LERG Arabidopsis thaliana genomic clone LERGI42, genomic survey sequence.

ACCESSION AQ962940

VERSION AQ962940.1 GI:6790641

KEYWORDS GSS.

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 169)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,

Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Genomic survey sequencing of Landsberg erecta ecotype of

Arabidopsis thaliana and identification of sequence-based

polymorphisms

Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: xt@tigr.org

For additional information, see <http://www.tigr.org/cdb/at/at.html>

Similar to A. thaliana chloroplast sequence (GB:AP000423)

Seq primer: TR

Class: shotgun.

FEATURES

source

Location/Qualifiers

1..169

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Landsberg erecta"

/db_xref="taxon:3702"

/clones="LERGI42"

/clone_lib="LERG"

/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was

sheared to 0.4-0.7 kbp before ligation."

ORIGIN

Query Match 48.3%; Score 30.4; DB 9; Length 169;
 Best Local Similarity 77.1%; Pred. No. 3.8;
 Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 118 GTGGGATTGACGTAGGGGCTAGGGTAGCTATATTCTGGAGCGAA 71
 |||||

RESULT 14
 BZ483881
 LOCUS BOOA129TR BO.1.6.2_KB tot Brassica oleracea genomic clone BOOA129,
 DEFINITION genomic survey sequence.
 ACCESSION BZ483881
 VERSION BZ483881.1 GI:26786279
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 183)
 AUTHORS Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
 Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
 TITLE Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
 JOURNAL Genome Res. 15 (4), 487-495 (2005)
 PUBMED 15805490
 COMMENT Other GSSs: BOOA129TF
 Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES

source
 1..183
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone_lib="BOOA129"
 /clone_lib="BO.1.6.2_KB_tot"
 /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
 total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 48.3%; Score 30.4; DB 9; Length 183;
 Best Local Similarity 77.1%; Pred. No. 3.9;
 Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 62 GTGGGATTGACGTAGGGGCTAGGGTAGCTATATTCTGGAGCGAA 109
 |||||

RESULT 15
 AQ962945/c
 LOCUS LERGI45TR LERG Arabidopsis thaliana genomic clone LERGI45, genomic
 DEFINITION survey sequence.
 ACCESSION AQ962945
 VERSION AQ962945.1 GI:6790646
 KEYWORDS GSS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 194)
 AUTHORS Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
 Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.
 TITLE Genomic survey sequencing of Landsberg erecta ecotype of
 Arabidopsis thaliana and identification of sequence-based
 polymorphisms
 JOURNAL Unpublished (2000)
 COMMENT Contact: Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: at@tigr.org
 For additional information, see http://www.tigr.org/tdb/at/at.html
 Seq primer: TR
 Class: Shotgun.

FEATURES
 source
 1..194
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone_lib="LERG"
 /note="Organ: Leaf; Vector: pUC19UK; Total genomic DNA was
 sheared to 0.4-0.7 kbp before ligation."

ORIGIN
 Query Match 48.3%; Score 30.4; DB 9; Length 194;
 Best Local Similarity 77.1%; Pred. No. 3.9;
 Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 137 GTGGGATTGACGTAGGGGCTAGGGTAGCTATATTCTGGAGCGAA 90
 |||||

Search completed: February 21, 2006, 07:16:42
 Job time : 3776 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:33:20 ; Search time 282 Seconds
(without alignments)
1488.921 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttctccgagtgagg.....gctattattagaggagcgaa 63

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9593994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseqn21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	13	ADT78252
2	38.4	61.0	112	13	ADT78220
3	38.4	61.0	112	13	ADT78224
4	38.4	61.0	112	13	ADT78219
5	36.6	58.1	112	13	ADT78211
6	34.8	55.2	112	13	ADT78210
7	33.6	53.3	91	9	ACC85363
8	33.6	53.3	91	10	AD834206
9	33.6	53.3	112	13	ADT78229
10	33.6	53.3	112	13	ADT78231
11	33.6	53.3	112	13	ADT78228
12	33.6	53.3	112	13	ADT78230
13	33.6	53.3	112	13	ADT78207
14	33.6	53.3	112	13	ADT78204
15	33.6	53.3	112	13	ADT78208
16	33.6	53.3	112	13	ADT78206
17	33.6	53.3	112	13	ADT78205
18	33.6	53.3	112	13	ADT78209
19	33.6	53.3	113	14	AEA36357

20	33.6	53.3	119	14	ADX17034
21	33.6	53.3	127	4	Aaf84276
22	33.6	53.3	129	2	AAX21430
23	33.6	53.3	140	2	AAX21424
24	33.6	53.3	142	6	ABS55361
25	33.6	53.3	150	2	AAX21406
26	33.6	53.3	161	2	AAX21423
27	33.6	53.3	164	2	AAX21431
28	33.6	53.3	165	2	AAX21409
29	33.6	53.3	168	2	AAX21407
30	33.6	53.3	168	3	AAZ88175
31	33.6	53.3	168	4	AAF25352
32	33.6	53.3	168	4	AAF57902
33	33.6	53.3	176	12	ADM01282
34	33.6	53.3	184	4	AAF89143
35	33.6	53.3	201	2	AAT66301
36	33.6	53.3	220	6	ABS54934
37	33.6	53.3	233	13	ADT78239
38	33.6	53.3	234	13	ADT78243
39	33.6	53.3	244	3	AAA47372
40	33.6	53.3	244	3	AAZ88176
41	33.6	53.3	244	4	AAF25353
42	33.6	53.3	244	4	AAF57903
43	33.6	53.3	258	2	AAX21429
44	33.6	53.3	804	10	ADE34327
45	33.6	53.3	1134	2	AAT85195

ALIGNMENTS

RESULT 1

ADT78252
ID ADT78252 standard; DNA; 63 BP.

XX AC ADT78252;

XX DT 27-JAN-2005 (first entry)

XX DE Mutant Prm promoter (Prm11)

XX DE useful for transgene expression in plants.

XX KW Heterologous molecule expression; plastid rRNA operon; Prm promoter;

XX KW transgenic plant; transgene expression;

XX KW Prm transcription modulating element; PTME; chimeric promoter; mutant;

XX KW ds.

XX OS Synthetic.

XX OS Unidentified.

XX PN US2004221338-A1.

XX PD 04-NOV-2004.

XX PF 15-DEC-2003; 2003US-00737251.

XX PR 13-DEC-2002; 2002US-0433302P.

XX PA (MALI/) MALIGA P.

XX PA (SUZU/) SUZUKI J Y.

XX PI Maliga P, Suzuki JY;

XX PI WPI; 2004-774976/76.

XX DR New isolated nucleic acid sequence, useful for promoting expression of

XX PT heterologous molecules in the plasmids of higher plants and for

XX PT constructing chimeric promoters for transgene expression.

XX PS Claim 7; SEQ ID NO 51; 34pp; English.

XX CC The invention relates to nucleic acid sequences for promoting expression

XX CC of heterologous molecules in the plasmids of higher plants. The nucleic

XX CC acid sequences are selected from plastid rRNA operon (Prm) sequences

CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a mutant Prn promoter that
 CC can be used to express heterologous molecules in the plastids of higher
 CC plants.
 XX
 SQ Sequence 63 BP; 13 A; 12 C; 24 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 13; Length 63;
 Best Local Similarity 100.0%; Pred. No. 8.1e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGCTCTTCTCCGAGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATTATTAGAGGAGC 60
 |||||
 DB 1 GAGCTCTTCTCCGAGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATTATTAGAGGAGC 60

OY 61 GAA 63
 |||
 DB 61 GAA 63

RESULT 2
 ADT78220
 ID ADT78220 standard; DNA; 112 BP.
 XX
 AC ADT78220;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE DNA sequence of Prn promoter derivative pJYS172.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.
 XX
 PN US2004221338-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX
 PI Maliga P, Suzuki JY;
 XX
 DR WPI; 2004-774976/76.
 XX

XX New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX
 XX
 PS Claim 1; SEQ ID NO 19; 34pp; English.
 CC
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic

CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX
 SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATTATTAGAGGAGCGAA 63
 |||||
 DB 28 GTGGATTGACGTGAGGGGGCAGGCTAGGCTATTATTCTGGAGCGAA 75

RESULT 3
 ADT78224
 ID ADT78224 standard; DNA; 112 BP.
 XX
 AC ADT78224;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE DNA sequence of Prn promoter derivative pJYS176.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.
 XX
 PN US2004221338-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX
 PI Maliga P, Suzuki JY;
 XX
 DR WPI; 2004-774976/76.
 XX
 PT New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX
 PS Claim 1; SEQ ID NO 23; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this

CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn promoter element, the chimeric
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX
 SQ Sequence 112 BP; 33 A; 16 C; 42 G; 21 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 28 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 75
 |||||

RESULT 4
 ADT78219
 ID ADT78219 standard; DNA; 112 BP.
 XX
 AC ADT78219;
 XX
 DT 27-JAN-2005 (first entry)
 DE DNA sequence of Prn promoter derivative pJYS171.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression;
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.

US2004221338-A1.
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX
 PI Maliga P, Suzuki JY;
 XX WPI; 2004-774976/76.
 XX
 PT New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.

PS Claim 1; SEQ ID NO 18; 34pp; English.
 XX
 CC The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn promoter element, the chimeric
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the

CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX
 SQ Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 Db 28 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 75
 |||||

RESULT 5
 ADT78211
 ID ADT78211 standard; DNA; 112 BP.
 XX
 AC ADT78211;
 XX
 DT 27-JAN-2005 (first entry)
 DE DNA sequence of Prn promoter derivative pJYS119.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression;
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.
 XX
 PN US2004221338-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX
 PI Maliga P, Suzuki JY;
 XX WPI; 2004-774976/76.
 XX
 PT New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.

PS Claim 1; SEQ ID NO 10; 34pp; English.
 XX
 CC The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn promoter element, the chimeric
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene

CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.

XX Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;

Query Match 58.1%; Score 36.6; DB 13; Length 112;
 Best Local Similarity 82.4%; Pred. No. 0.00074;
 Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 13 GAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 25 GAGGTGGGATTGACGTGAGGGGGCAGGGATGCTATATTCTGGAGCGAA 75
 |||||

RESULT 6

ADT78210
 ID ADT78210 standard; DNA; 112 BP.

AC ADT78210;

DT 27-JAN-2005 (first entry)

XX DNA sequence of Prn promoter derivative pJYS118.

DE Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression;
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.

XX Unidentified.

OS US2004221338-A1.

XX 04-NOV-2004.

PF 15-DEC-2003; 2003US-00737251.

XX 13-DEC-2002; 2002US-0433302P.

PR (MALI/) MALIGA P.

PA (SUZU/) SUZUKI J Y.

XX Maliga P, Suzuki JY;

PI WPI; 2004-774976/76.

XX New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.

PS Claim 1; SEQ ID NO 9; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.

XX Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;

Query Match 55.2%; Score 34.8; DB 13; Length 112;
 Best Local Similarity 77.8%; Pred. No. 0.0035;
 Matches 42; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 10 TCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 22 TCCCTCGTGGGATTGACGTGAGGGGGCAGGGATGCTATATTCTGGAGCGAA 75
 |||||

RESULT 7

ACC85363
 ID ACC85363 standard; DNA; 91 BP.

XX ACC85363;

DT 18-SEP-2003 (first entry)

DE N tabacum Prn16 promoter.

XX Vegetable plastid transformation; transgenic; recognition sequence;
 KW plant; site-specific integration; nutrition; seed production; gene;
 KW chemical production; promoter; ds.

XX Nicotiana tabacum.

XX WO2003054201-A1.

XX 03-JUL-2003.

XX 16-DEC-2002; 2002WO-EP014303.

XX 20-DEC-2001; 2001DE-01063159.

XX (SUNG-) SUNGENE GMBH & CO KGAA.

XX Biesgen C;

XX WPI; 2003-541820/51.

PT Site-specific integration of DNA into plastid DNA, useful for making
 PT transgenic plants used e.g. as food, by recombinase-mediated insertion.

PS Disclosure; Page 132; 164pp; German.

XX The present invention relates to a method for the site-specific
 CC integration of a DNA sequence into the plastid DNA of a plant or its
 CC derived cells. Transgenic plants in which a DNA sequence has been
 CC integrated, also their cell cultures, organs, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a gene fragment shown in the exemplification of the
 CC invention

XX Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;

Query Match 53.3%; Score 33.6; DB 9; Length 91;
 Best Local Similarity 81.2%; Pred. No. 0.0096;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 |||||
 DB 34 GTGGGATTGACGTGAGGGGGCAGGGATGCTATATTCTGGAGCGAA 81
 |||||

RESULT 8

ADE34206

ID ADE34206 standard; DNA; 91 BP.

XX ADE34206;

XX 29-JAN-2004 (first entry)

DE XX Tobacco Prn16 promoter DNA.

KW XX plastid; plant; homotransplastomic cell; insertion sequence; nutrition;

KW XX seed production; enzyme; vitamin; amino acid; flavouring;

KW XX aromatising agent; dye; antibody; vaccine; ds.

XX XX Nicotiana tabacum.

XX XX WO2003054189-A2.

XX XX 03-JUL-2003.

XX XX 16-DEC-2002; 2002WO-EP014302.

XX XX 20-DEC-2001; 2001DE-01063161.

XX XX (SUNG-) SUNGENE GMBH & CO KGAA.

XX XX Biesgen C;

XX XX WPI; 2003-541816/51.

XX XX Method for integrating DNA into plant plastids, useful for making

PT transgenic plants for e.g. food or animal feed, by inducing targeted

PT double-strand DNA breaks.

XX XX Disclosure; SEQ ID NO 46; 182pp; German.

XX XX This invention describes a novel method for integrating a DNA sequence

CC into the plastid DNA of a multicellular plant or its derived cells and

CC for selecting homotransplastomic cells or plants. The method comprises

CC inducing DNA double-strand breaks in plant plastid DNA, which contains at

CC least one recognition site for targeted induction of such breaks, by

CC treating the plant or its cells with an enzyme able to create these

CC breaks and a transformation construct that contains an insertion sequence

CC which is inserted into the plastid DNA so that the function of the

CC recognition site for targeted induction of breaks is inactivated, i.e. it

CC is no longer cleaved by the enzyme. Plants or cells in which the

CC insertion sequence has been inserted are then selected. Transgenic plants

CC in which the DNA sequence has been integrated, and also their cell

CC cultures, organs, tissues, are useful in human or animal nutrition, for

CC producing seeds, and pharmaceuticals or fine chemicals, e.g. enzymes,

CC vitamins, amino acids, flavourings and aromatising agents, dyes,

CC antibiotics and vaccines. The method eliminates the need for

CC antibiotic/herbicide selection markers and ensures efficient integration

CC of foreign DNA into all copies of plastid DNA, also effective selection,

CC so provides a quicker, more efficient and less expensive method of

CC producing homotransplastomic plants. The genetic constructs used are

CC small, since only short homology regions are required. Double-crossover

CC events occur easily in plastid DNA, at specific locations, avoiding the

CC problems of gene silencing associated with recombination in the nucleus

CC and high level expression can be achieved, because of the high copy

CC number of plastid DNA. Foreign DNA will not be transferred in pollen

CC (inheritance of plastid DNA is maternal) and since plastids resemble

CC prokaryotes, they can express several genes from polycistronic operons,

XX under control of a single promoter.

XX XX Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;

SQ Query Match 53.3%; Score 33.6; DB 10; Length 91;

Best Local Similarity 81.2%; Pred. No. 0.0096;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

DB 34 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCTGGAGCGAA 81

RESULT 9

ADT78229

ID ADT78229 standard; DNA; 112 BP.

XX XX

AC ADT78229;

XX 27-JAN-2005 (first entry)

XX DNA sequence of Prn promoter derivative pJYS181.

XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;

XX transgenic plant; transgene expression;

XX Prn transcription modulating element; PTME; chimeric promoter; ds.

XX Unidentified.

XX US2004221338-A1.

XX 04-NOV-2004.

XX 15-DEC-2003; 2003US-00737251.

XX 13-DEC-2002; 2002US-0433302P.

XX (MALI/) MALIGA P.

XX (SUZU/) SUZUKI J Y.

XX Maliga P, Suzuki JY;

XX WPI; 2004-774976/76.

XX New isolated nucleic acid sequence, useful for promoting expression of

PT heterologous molecules in the plastids of higher plants and for

PT constructing chimeric promoters for transgene expression.

XX Claim 1; SEQ ID NO 28; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression

CC of heterologous molecules in the plastids of higher plants. The nucleic

CC acid sequences are selected from plastid rRNA operon (Prn) sequences

CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise

CC mutations which minimise homologous recombination at the Prn operon

CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the

CC nucleic acid sequence above, (b) a transgenic plant comprising this

CC vector, (c) a chimeric promoter for expression of transgenes in plastids

CC of higher plants, comprising at least one Prn transcription modulating

CC element (PTME) operably linked to a promoter element, the chimeric

CC promoter being further operably linked to a sequence encoding a

CC heterologous molecule of interest, and (d) a vector comprising the

CC chimeric promoter. The nucleic acid sequence is operably linked to a

CC sequence encoding a heterologous molecule of interest or its precursor.

CC Expression of the heterologous molecule is decreased or increased

CC relative to that observed using wild-type Prn sequence. The nucleic acid

CC sequence is useful for constructing chimeric promoters for transgene

CC expression and for driving high level expression of heterologous proteins

CC in plastids. The present sequence represents a Prn promoter derivative.

XX XX Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

SQ Query Match 53.3%; Score 33.6; DB 13; Length 112;

Best Local Similarity 81.2%; Pred. No. 0.01;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCTGGAGCGAA 75

RESULT 10

ADT78231

ID ADT78231 standard; DNA; 112 BP.

XX XX

AC ADT78231;

XX XX

DT 27-JAN-2005 (first entry)

XX XX

DE DNA sequence of Prn promoter derivative pJYS183.

XX XX

KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.
 OS Unidentified.
 XX US2004221338-A1.
 PN 04-NOV-2004.
 XX 15-DEC-2003; 2003US-00737251.
 XX 13-DEC-2002; 2002US-0433302P.
 PD (MALI/) MALIGA P.
 XX (SUZU/) SUZUKI J Y.
 XX Maliga P, Suzuki JY;
 XX WPI; 2004-774976/76.
 XX New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX Claim 1; SEQ ID NO 30; 34pp; English.
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or increased
 CC expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX SQ Sequence 112 BP; 30 A; 17 C; 41 G; 24 T; 0 U; 0 Other;
 Query Match 53.3%; Score 33.6; DB 13; Length 112;
 Best Local Similarity 81.2%; Pred. No. 0.01;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 Db 28 GTGGGATTGACGTGAGGGGGCGAGGATGCTATATTCTTGGGAGCGAA 75
 RESULT 11
 ADT78228
 ID ADT78228 standard; DNA; 112 BP.
 XX AC ADT78228;
 XX 27-JAN-2005 (first entry)
 DT DNA sequence of Prn promoter derivative pJYS180.
 DE Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 XX Unidentified.

XX US2004221338-A1.
 PN 04-NOV-2004.
 XX 15-DEC-2003; 2003US-00737251.
 XX 13-DEC-2002; 2002US-0433302P.
 PD (MALI/) MALIGA P.
 XX (SUZU/) SUZUKI J Y.
 XX Maliga P, Suzuki JY;
 XX WPI; 2004-774976/76.
 XX New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX Claim 1; SEQ ID NO 27; 34pp; English.
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or increased
 CC expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX SQ Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;
 Query Match 53.3%; Score 33.6; DB 13; Length 112;
 Best Local Similarity 81.2%; Pred. No. 0.01;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
 Db 28 GTGGGATTGACGTGAGGGGGCGAGGATGCTATATTCTTGGGAGCGAA 75
 RESULT 12
 ADT78230
 ID ADT78230 standard; DNA; 112 BP.
 XX AC ADT78230;
 XX 27-JAN-2005 (first entry)
 DT DNA sequence of Prn promoter derivative pJYS182.
 DE Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 XX Unidentified.
 XX US2004221338-A1.
 XX 04-NOV-2004.

PF 15-DEC-2003; 2003US-00737251.
 PR 13-DEC-2002; 2002US-0433302P.
 XX (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX Maliga P, Suzuki JY;
 PT WPI; 2004-774976/76.
 DR New isolated nucleic acid sequence, useful for promoting expression of
 XX heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX Claim 1; SEQ ID NO 29; 34pp; English.
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
 Query Match 53.3%; Score 33.6; DB 13; Length 112;
 Best Local Similarity 81.2%; Pred. No. 0.01;
 Matches 38; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTGGATTGACGTGAGGGGGTCCCTAGGCTATATTAGAGGACGAA 63
 DB 28 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTCTGGAGCGAA 75
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 ADT78207
 ID ADT78207 standard; DNA; 112 BP.
 XX AC ADT78207;
 XX 27-JAN-2005 (first entry)
 DE DNA sequence of Prn promoter derivative pUYS115.
 XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression;
 XX Prn transcription modulating element; PTME; chimeric promoter; ds.
 OS Unidentified.
 XX US2004221338-A1.
 PN 04-NOV-2004.
 XX 15-DEC-2003; 2003US-00737251.
 PR 13-DEC-2002; 2002US-0433302P.
 XX (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX Maliga P, Suzuki JY;
 PT WPI; 2004-774976/76.
 DR New isolated nucleic acid sequence, useful for promoting expression of
 XX heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX Claim 1; SEQ ID NO 29; 34pp; English.
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
 Query Match 53.3%; Score 33.6; DB 13; Length 112;
 Best Local Similarity 81.2%; Pred. No. 0.01;
 Matches 38; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTGGATTGACGTGAGGGGGTCCCTAGGCTATATTAGAGGACGAA 63
 DB 28 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTCTGGAGCGAA 75
 RESULT 14
 ADT78204
 ID ADT78204 standard; DNA; 112 BP.
 XX AC ADT78204;
 XX 27-JAN-2005 (first entry)
 DE DNA sequence of Prn promoter derivative pUYS112.
 XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;
 KW transgenic plant; transgene expression;
 XX Prn transcription modulating element; PTME; chimeric promoter; ds.
 OS Unidentified.
 XX US2004221338-A1.
 PN 04-NOV-2004.
 XX 15-DEC-2003; 2003US-00737251.
 PR 13-DEC-2002; 2002US-0433302P.
 XX (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 XX Maliga P, Suzuki JY;
 PT WPI; 2004-774976/76.
 DR New isolated nucleic acid sequence, useful for promoting expression of
 XX heterologous molecules in the plastids of higher plants and for
 PT constructing chimeric promoters for transgene expression.
 XX Claim 1; SEQ ID NO 6; 34pp; English.
 XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
 CC mutations which minimise homologous recombination at the Prn operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one Prn transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC heterologous molecule of interest, and (d) a vector comprising the
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type Prn sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a Prn promoter derivative.
 XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
 Query Match 53.3%; Score 33.6; DB 13; Length 112;
 Best Local Similarity 81.2%; Pred. No. 0.01;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTGGATTGACGTGAGGGGGTCCCTAGGCTATATTAGAGGACGAA 63
 DB 28 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTCTGGAGCGAA 75

XX New isolated nucleic acid sequence, useful for promoting expression of
PT heterologous molecules in the plastids of higher plants and for
PT constructing chimeric promoters for transgene expression.
XX
PS Disclosure; SEQ ID NO 3; 34pp; English.
XX
CC The invention relates to nucleic acid sequences for promoting expression
CC of heterologous molecules in the plastids of higher plants. The nucleic
CC acid sequences are selected from plastid rRNA operon (Prn) sequences
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
CC mutations which minimise homologous recombination at the Prn operon
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
CC nucleic acid sequence above, (b) a transgenic plant comprising this
CC vector, (c) a chimeric promoter for expression of transgenes in plastids
CC of higher plants, comprising at least one Prn transcription modulating
CC element (PTME) operably linked to a promoter element, the chimeric
CC promoter being further operably linked to a sequence encoding a
CC heterologous molecule of interest, and (d) a vector comprising the
CC chimeric promoter. The nucleic acid sequence is operably linked to a
CC sequence encoding a heterologous molecule of interest or its precursor.
CC Expression of the heterologous molecule is decreased or increased
CC relative to that observed using wild-type Prn sequence. The nucleic acid
CC sequence is useful for constructing chimeric promoters for transgene
CC expression and for driving high level expression of heterologous proteins
CC in plastids. The present sequence represents a Prn promoter derivative.
XX
SQ Sequence 112 BP; 31 A; 17 C; 41 G; 23 T; 0 U; 0 Other;

Query Match 53.3%; Score 33.6; DB 13; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTTGGGAGCGAA 75

RESULT 15
ADT78208
ID ADT78208 standard; DNA; 112 BP.
XX
AC ADT78208;
XX
DT 27-JAN-2005 (first entry)
XX
DE DNA sequence of Prn promoter derivative pJYS116.
XX
KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
KW transgenic plant; transgene expression;
KW Prn transcription modulating element; PTME; chimeric promoter; ds.
XX
OS Unidentified.
XX
XX US2004221338-A1.
XX
PD 04-NOV-2004.
XX
XX 15-DEC-2003; 2003US-00737251.
XX
PR 13-DEC-2002; 2002US-0433302P.
XX
PA (MALI/) MALIGA P.
PA (SUZU/) SUZUKI J Y.
XX
PI Maliga P, Suzuki JY;
XX
XX WPI; 2004-774976/76.
XX
XX New isolated nucleic acid sequence, useful for promoting expression of
PT heterologous molecules in the plastids of higher plants and for
PT constructing chimeric promoters for transgene expression.
XX

PS Claim 1; SEQ ID NO 7; 34pp; English.
XX
CC The invention relates to nucleic acid sequences for promoting expression
CC of heterologous molecules in the plastids of higher plants. The nucleic
CC acid sequences are selected from plastid rRNA operon (Prn) sequences
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
CC mutations which minimise homologous recombination at the Prn operon
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
CC nucleic acid sequence above, (b) a transgenic plant comprising this
CC vector, (c) a chimeric promoter for expression of transgenes in plastids
CC of higher plants, comprising at least one Prn transcription modulating
CC element (PTME) operably linked to a promoter element, the chimeric
CC promoter being further operably linked to a sequence encoding a
CC heterologous molecule of interest, and (d) a vector comprising the
CC chimeric promoter. The nucleic acid sequence is operably linked to a
CC sequence encoding a heterologous molecule of interest or its precursor.
CC Expression of the heterologous molecule is decreased or increased
CC relative to that observed using wild-type Prn sequence. The nucleic acid
CC sequence is useful for constructing chimeric promoters for transgene
CC expression and for driving high level expression of heterologous proteins
CC in plastids. The present sequence represents a Prn promoter derivative.
XX
SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

Query Match 53.3%; Score 33.6; DB 13; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTTGGGAGCGAA 75

Search completed: February 21, 2006, 05:38:11
Job time : 283 secs

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:35:59 ; Search time 2168 Seconds
(without alignments)
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Title: US-10-737-251-51
Perfect score: 63
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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1: gb_ba.*
2: gb_in.*
3: gb_env.*
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6: gb_pat.*
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14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	91	6	AX798146 Sequence
2	33.6	53.3	91	6	AX798954 Sequence
3	33.6	53.3	113	6	CS114516 Sequence
4	33.6	53.3	119	15	CS001461 Sequence
5	33.6	53.3	127	6	ES1179 Method for
6	33.6	53.3	127	6	ES1197 Process for
7	33.6	53.3	127	6	AR39398 Sequence
8	33.6	53.3	127	6	AX137514 Sequence
9	33.6	53.3	142	6	BD174932 A system
10	33.6	53.3	168	6	AX076661 Sequence
11	33.6	53.3	176	6	CQ797808 Sequence
12	33.6	53.3	184	6	AR145914 Sequence
13	33.6	53.3	201	6	AR242682 Sequence
14	33.6	53.3	202	6	AR568182 Sequence
15	33.6	53.3	202	6	AX076662 Sequence
16	33.6	53.3	202	6	AX319835 Sequence
17	33.6	53.3	210	15	AF189150 Gossypium
18	33.6	53.3	220	6	BD180933 Method of

19	33.6	53.3	220	6	AX537601 Sequence
20	33.6	53.3	244	6	BD247598 Methods f
21	33.6	53.3	244	6	AR568183 Sequence
22	33.6	53.3	244	6	AX319836 Sequence
23	33.6	53.3	300	6	AR171710 Sequence
24	33.6	53.3	300	6	AR171711 Sequence
25	33.6	53.3	553	6	CQ828073 Sequence
26	33.6	53.3	557	15	DCCLGTRV
27	33.6	53.3	762	15	CPHATV
28	33.6	53.3	804	6	AX798912 Sequence
29	33.6	53.3	1143	6	AR368829 Sequence
30	33.6	53.3	1148	6	CQ830289 Sequence
31	33.6	53.3	1183	6	BD235370 Translati
32	33.6	53.3	1293	6	CQ793220 Sequence
33	33.6	53.3	1293	6	CS039141 Sequence
34	33.6	53.3	1327	6	CQ828069 Sequence
35	33.6	53.3	1330	6	CQ828070 Sequence
36	33.6	53.3	1332	6	CQ830287 Sequence
37	33.6	53.3	1359	6	AX798126 Sequence
38	33.6	53.3	1359	6	AX798910 Sequence
39	33.6	53.3	1417	6	AR368830 Sequence
40	33.6	53.3	1487	6	CQ828074 Sequence
41	33.6	53.3	1613	6	CQ830293 Sequence
42	33.6	53.3	1694	6	CQ828072 Sequence
43	33.6	53.3	1746	6	CQ828071 Sequence
44	33.6	53.3	2113	15	CHNTRN1
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ALIGNMENTS

RESULT 1
AX798146
LOCUS AX798146
DEFINITION Sequence 22 from Patent WO03054201.
ACCESSION AX798146
VERSION AX798146.1 GI:37604427
KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE 1
AUTHORS Biesgen,C.
TITLE Method for the transformation of vegetable plastids
JOURNAL Patent: WO 03054201-A 22 03-JUL-2003;
Sungene GmbH & Co. KGAA (DE)
FEATURES Location/Qualifiers
source 1..91
/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
promoter 1..91
/note="plastidic promoter Prn16"

ORIGIN
Query Match 53.3%; Score 33.6; DB 6; Length 91;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 34 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 81

RESULT 2
AX798954
LOCUS AX798954
DEFINITION Sequence 46 from Patent WO03054189.
ACCESSION AX798954
VERSION AX798954.1 GI:37605006

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KEYWORDS      Nicotiana tabacum (common tobacco)
SOURCE
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS      Biesgen, C.
TITLE        Methods for the transformation of vegetal plastids
JOURNAL      Patent: WO 03054189-A 46 03-JUL-2003;
               Sungene GmbH & Co. KGAA (DE)
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source       1..91
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               /db_xref="taxon:4097"
promoter     1..91
               /note="plastidic promoter Prn16"
ORIGIN
Query Match  53.3%; Score 33.6; DB 6; Length 91;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 34 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 81

RESULT 3
LOCUS      CS114516 113 bp DNA linear PAT 24-JUN-2005
DEFINITION Sequence 13 from Patent WO2005054481.
ACCESSION  CS114516
VERSION     CS114516.1 GI:68226041
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE
AUTHORS    Muehlbauer, S.
TITLE      Controlling gene expression in plastids
JOURNAL    Patent: WO 2005054481-A 13 16-JUN-2005;
               Icon Genetics AG (DE)
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source     1..113
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               /note="cloning oligo"
ORIGIN
Query Match  53.3%; Score 33.6; DB 6; Length 113;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 38 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 85

RESULT 4
LOCUS      CS001461 119 bp DNA linear PLN 01-FEB-2005
DEFINITION Sequence 6 from Patent WO2005005643.
ACCESSION  CS001461
VERSION     CS001461.1 GI:58423938
KEYWORDS   Nicotiana tabacum (common tobacco)
SOURCE     Nicotiana tabacum
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS      Cox, K.M. and Peele, C.G.
TITLE        Chloroplast transformation of duckweed
JOURNAL      Patent: WO 2005005643-A 20-JAN-2005;
               Biolex, Inc. (US)
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source       1..119
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Query Match  53.3%; Score 33.6; DB 15; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 41 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 88

RESULT 5
LOCUS      E51179 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION  E51179
VERSION     E51179.1 GI:18629496
KEYWORDS   Nicotiana tabacum (common tobacco)
SOURCE     Nicotiana tabacum
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS      Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE        Method for transforming plant and transformed plant
JOURNAL      Patent: JP 2001046073-A 16 20-FEB-2001;
               RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT     OS Nicotiana tabacum (tobacco)
               PN JP 2001046073-A/16
               PD 20-FEB-2001
               PF 09-AUG-1999 JP 1999225832
               PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
               PI C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC
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Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 53 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 100

RESULT 6
LOCUS      E51197 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing polyester.
ACCESSION  E51197
VERSION     E51197.1 GI:18629514
KEYWORDS   JP 2001046074-A/16.

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SOURCE
ORGANISM      Nicotiana tabacum (common tobacco)
REFERENCE
AUTHORS       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL       asterids; lamids; Solanales; Solanaceae; Nicotiana.
COMMENT       1 (bases 1 to 127)
              Nakashita,H., Yamaguchi,I., Yoshioka,K. and Doi,Y.
              Process for producing polyester
              Patent: JP 2001046074-A 16 20-FEB-2001;
              RIKAGAKU KENKYUSHO
OS            Nicotiana tabacum (tobacco)
PN            JP 2001046074-A/16
PD            20-FEB-2001
PF            09-AUG-1999 JP 1999225839
PR            HI DEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIOHARU DOI
PC            C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N5/10,C12P7/62, PC
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source
Query Match 53.3%; Score 33.6; DB 6; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
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RESULT 7
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LOCUS        AR399398 127 bp DNA linear PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6620601.
ACCESSION   AR399398
VERSION     AR399398.1 GI:40141264
KEYWORDS    Unknown.
SOURCE      Uncloned.
ORGANISM    Uncloned.
REFERENCE
AUTHORS     Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
TITLE       Methods for transformation of plants, transformed plants and
JOURNAL     processes for preparation of polyesters
            Patent: US 6620601-A 16 16-SEP-2003;
            Riken; Saitama;
            JPX;
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Best Local Similarity 81.2%; Pred. No. 0.097;
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AX137514
LOCUS        AX137514 127 bp DNA linear PAT 30-MAY-2001
DEFINITION  Sequence 16 from Patent EP1076095.
ACCESSION   AX137514
VERSION     AX137514.1 GI:14273708
KEYWORDS    Nicotiana tabacum (common tobacco)
ORGANISM    Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
Methods for transformation of plants, transformed plants and
processes for preparation of polyesters
Patent: EP 1076095-A 16 14-FEB-2001;
Riken (JP)
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Query Match 53.3%; Score 33.6; DB 6; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
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DEFINITION  Sequence 16 from Patent EP1076095.
ACCESSION   AX137514
VERSION     AX137514.1 GI:14273708
KEYWORDS    Nicotiana tabacum (common tobacco)
ORGANISM    Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
Methods for transformation of plants, transformed plants and
processes for preparation of polyesters
Patent: EP 1076095-A 16 14-FEB-2001;
Riken (JP)
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Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
ORIGIN
16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
53 GTGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGAGCGAA 100
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BD174932
LOCUS        BD174932 142 bp DNA linear PAT 18-MAR-2003
DEFINITION  A system for expressing protein using plants.
ACCESSION   BD174932
VERSION     BD174932.1 GI:29120626
KEYWORDS    JP 2002272476-A/2.
SOURCE      Nicotiana tabacum (common tobacco)
ORGANISM    Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 142)
Tomizawa,K. and Yokota,A.
A system for expressing protein using plants
Patent: JP 2002272476-A 2 24-SEP-2002;
RESEARCH INSTITUTE OF INNOVATIVE TECHNOLOGY FOR THE EARTH
OS            Nicotiana tabacum (tobacco)
PN            JP 2002272476-A/2
PD            24-SEP-2002
PF            22-MAR-2001 JP 2001083569
PI            KENICHI TOMIZAWA, AKIHO YOKOTA
PC            C12N15/09,A01H5/00,C07K14/415,C12N5/10,C12N5/00,C12N5/00 CC
rrn promoter
FH            Key Location/Qualifiers
FT            1. .142
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              /db_xref="taxon:4097"
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Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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RESULT 10
AX076661
LOCUS AX076661 168 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 1 from Patent WO0104331.
ACCESSION AX076661
VERSION AX076661.1 GI:12711193
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE
1 Staub,J.M.
AUTHORS Enhanced expression of proteins using gfp
TITLE Patent: WO 0104331-A 1 18-JAN-2001;
JOURNAL Calgene LLC (US)
FEATURES
source
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 53.3%; Score 33.6; DB 6; Length 168;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 63 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGAGCGAA 110
RESULT 11
CQ797808
LOCUS CQ797808 176 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 14 from Patent WO2004029256.
ACCESSION CQ797808
VERSION CQ797808.1 GI:46426081
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.
AUTHORS and ramos gonz lez O.
TITLE Vector for the production of transplastomic angiosperm plants
JOURNAL Patent: WO 2004029256-A 14 08-APR-2004;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Synthetic DNA
fragment coding for the promoter region of the plastid
16S ribosomal RNA (Prn), with added restriction sites."
ORIGIN
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Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 56 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGAGCGAA 103
RESULT 12
AR145914
LOCUS AR145914 184 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6218145.
ACCESSION AR145914
VERSION AR145914.1 GI:15109103
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 184)
AUTHORS Bogosian,G., O'Neil,J.P. and Staub,J.M.
TITLE Bacterial expression systems based on plastic or mitochondrial
promoter combinations
JOURNAL Patent: US 6218145-A 3 17-APR-2001;
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Location/Qualifiers
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/organism="unknown"
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Query Match 53.3%; Score 33.6; DB 6; Length 184;
Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 42 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGAGCGAA 89
RESULT 13
AR242682
LOCUS AR242682 201 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 58 from patent US 6472586.
ACCESSION AR242682
VERSION AR242682.1 GI:27289157
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 201)
AUTHORS Maliga,P., Allison,L.A. and Hajdukiewicz,P.T.
TITLE Nuclear-encoded transcription system in plastids of higher plants
JOURNAL Patent: US 6472586-A 58 29-OCT-2002;
Rutgers, The State University of New Jersey; Piscataway, NJ
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Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 45 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGAGCGAA 92
RESULT 14
AR568182
LOCUS AR568182 202 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6781033.
ACCESSION AR568182
VERSION AR568182.1 GI:53986476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 202)
AUTHORS Staub,J.M., Ye,G. and Broyles,D.L.
TITLE Method for the transformation of plant cell plastids
JOURNAL Patent: US 6781033-A 1 24-AUG-2004;
Monsanto Technology LLC; St. Louis, MO;
WOX;
FEATURES
source
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Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN

Query Match 53.3%; Score 33.6; DB 6; Length 202;
Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 45 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTTCTGGAGCGAA 92

RESULT 15

AX076662
LOCUS AX076662 202 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 2 from Patent WO0104331.

ACCESSION AX076662

VERSION AX076662.1 GI:12711194

KEYWORDS

SOURCE

ORGANISM

synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

AUTHORS

TITLE

Enhanced expression of proteins using gfp

JOURNAL

Patent: WO 0104331-A 2 18-JAN-2001;

Calgene LLC (US)

FEATURES

Location/Qualifiers

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 53.3%; Score 33.6; DB 6; Length 202;
Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
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Db 45 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTTCTGGAGCGAA 92

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